



## SEQUENCE LISTING

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MICHAEL HOUGHTON  
MANMOHAN SINGH

<120> COMPOSITIONS COMPRISING CATIONIC MICROPARTICLES  
AND HCV E1E2 DNA AND METHODS OF USE THEREOF

<130> PP020407.0004

<140> 10/554, 625

<141> 2007-03-21

<150> 60/465, 841

<151> 2003-04-25

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 1914

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region

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<221> CDS

<222> (1)..(1911)

<400> 1

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tct ttc tct atc ttc ctt ctg gcc ctg ctc tct tgc ttg act gtg ccc
Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro
   1           5           10          15

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gct tcg gcc tac caa gtg cgc aac tcc acg ggg ctc tac cac gtc acc 96  
 Ala Ser Ala Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr  
                   20                  25                  30

```

aat gat tgc cct aac tcg agt att gtg tac gag gcg gcc gat gcc atc 144
Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile
          35           40           45

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ctg cac act ccg ggg tgc gtc cct tgc gtt cgc gag ggc aac gcc tcg 192  
 Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser  
       50              55              60

```

agg tgt tgg gtg gcg atg acc cct acg gtg gcc acc agg gat ggc aaa 240
Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys
   65          70          75          80

```

ctc ccc gcg acg cag ctt cga cgt cac atc gat ctg ctt gtc ggg agc 288  
 Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
                   85                  90                  95

```
gcc acc ctc tgt tcg gcc ctc tac gtg ggg gac ctg tgc ggg tct gtc 336
Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val
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100	105	110	
ttt ctt gtc ggc caa ctg ttt acc ttc tct ccc agg cgc cac tgg acg Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr			384
115	120	125	
acg caa ggt tgc aat tgc tct atc tat ccc ggc cat ata acg ggt cac Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His			432
130	135	140	
cgc atg gca tgg gat atg atg aac tgg tcc cct acg acg gcg ttg Arg Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu			480
145	150	155	160
gta atg gct cag ctg ctc cg <sup>g</sup> atc cca caa gcc atc ttg gac atg atc Val Met Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile			528
165	170	175	
gct ggt gct cac tgg gga gtc ctg gcg ggc ata gcg tat ttc tcc atg Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met			576
180	185	190	
gtg ggg aac tgg gcg aag gtc ctg gta gtg ctg ctg cta ttt gcc ggc Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Phe Ala Gly			624
195	200	205	
gtc gac gcg gaa acc cac gtc acc ggg gga agt gcc ggc cac act gtg Val Asp Ala Glu Thr His Val Thr Gly Gly Ser Ala Gly His Thr Val			672
210	215	220	
tct gga ttt gtt agc ctc ctc gca cca ggc gcc aag cag aac gtc cag Ser Gly Phe Val Ser Leu Leu Ala Pro Gly Ala Lys Gln Asn Val Gln			720
225	230	235	240
ctg atc aac acc aac ggc agt tgg cac ctc aat agc acg gcc ctg aac Leu Ile Asn Thr Asn Gly Ser Trp His Leu Asn Ser Thr Ala Leu Asn			768
245	250	255	
tgc aat gat agc ctc aac acc ggc tgg ttg gca ggg ctt ttc tat cac Cys Asn Asp Ser Leu Asn Thr Gly Trp Leu Ala Gly Leu Phe Tyr His			816
260	265	270	
cac aag ttc aac tct tca ggc tgt cct gag agg cta gcc agc tgc cga His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg			864
275	280	285	
ccc ctt acc gat ttt gac cag ggc tgg ggc cct atc agt tat gcc aac Pro Leu Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn			912
290	295	300	
gga agc ggc ccc gac cag cgc ccc tac tgc tgg cac tac ccc cca aaa Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro Pro Lys			960
305	310	315	320
cct tgc ggt att gtg ccc gcg aag agt gtg tgt ggt ccg gta tat tgc Pro Cys Gly Ile Val Pro Ala Lys Ser Val Cys Gly Pro Val Tyr Cys			1008
325	330	335	
ttc act ccc agc ccc gtg gtg gga acg acc gac agg tcg ggc gcg Phe Thr Pro Ser Pro Val Val Gly Thr Thr Asp Arg Ser Gly Ala			1056

340	345	350	
ccc acc tac agc tgg ggt gaa aat gat acg gac gtc ttc gtc ctt aac Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val Leu Asn 355	360	365	1104
aat acc agg cca ccg ctg ggc aat tgg ttc ggt tgt acc tgg atg aac Asn Thr Arg Pro Pro Leu Gly Asn Trp Phe Gly Cys Thr Trp Met Asn 370	375	380	1152
tca act gga ttc acc aaa gtg tgc gga gcg cct cct tgt gtc atc gga Ser Thr Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile Gly 385	390	395	1200
ggg gcg ggc aac aac acc ctg cac tgc ccc act gat tgc ttc cgc aag Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Phe Arg Lys 405	410	415	1248
cat ccg gac gcc aca tac tct cgg tgc ggc tcc ggt ccc tgg atc aca His Pro Asp Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr 420	425	430	1296
ccc agg tgc ctg gtc gac tac ccg tat agg ctt tgg cat tat cct tgt Pro Arg Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys 435	440	445	1344
acc atc aac tac act ata ttt aaa atc agg atg tac gtg gga ggg gtc Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly Gly Val 450	455	460	1392
gag cac agg ctg gaa gct gcc tgc aac tgg acg cgg ggc gaa cgt tgc Glu His Arg Leu Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys 465	470	475	1440
gat ctg gaa gat agg gac agg tcc gag ctc agc ccg tta ctg ctg acc Asp Leu Glu Asp Arg Asp Ser Glu Leu Ser Pro Leu Leu Leu Thr 485	490	495	1488
act aca cag tgg cag gtc ctc ccg tgt tcc ttc aca acc ctg cca gcc Thr Thr Gln Trp Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala 500	505	510	1536
ttg tcc acc ggc ctc atc cac ctc cac cag aac att gtg gac gtg cag Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln 515	520	525	1584
tac ttg tac ggg gtg ggg tca agc atc gcg tcc tgg gcc att aag tgg Tyr Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp 530	535	540	1632
gag tac gtc gtc ctc ctg ttc ctt ctg ctt gca gac gcg cgc gtc tgc Glu Tyr Val Val Leu Leu Phe Leu Leu Ala Asp Ala Arg Val Cys 545	550	555	1680
tcc tgc ttg tgg atg atg cta ctc ata tcc caa gcg gaa gcg gct ttg Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu 565	570	575	1728
gag aac ctc gta ata ctt aat gca gca tcc ctg gcc ggg acg cac ggt Glu Asn Leu Val Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly 580	585	590	1776

ctt gta tcc ttc ctc gtg ttc ttc tgc ttt gca tgg tat ctg aag ggt      1824  
 Leu Val Ser Phe Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly  
  595                        600                        605  
  
 aag tgg gtg ccc gga gcg gtc tac acc ttc tac ggg atg tgg cct ctc      1872  
 Lys Trp Val Pro Gly Ala Val Tyr Thr Phe Tyr Gly Met Trp Pro Leu  
  610                        615                        620  
  
 ctc ctg ctc ctg ttg gcg ttg ccc cag cg<sup>g</sup> tac gcg taa      1914  
 Leu Leu Leu Leu Ala Leu Pro Gln Arg Ala Tyr Ala  
  625                        630                        635  
  
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 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region  
  
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 Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro  
  1                        5                            10                        15  
  
 Ala Ser Ala Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr  
  
  20                        25                        30  
  
 Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile  
  35                        40                        45  
  
 Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser  
  50                        55                        60  
  
 Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys  
  65                        70                        75                        80  
  
 Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
  85                        90                        95  
  
 Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val  
  100                        105                        110  
  
 Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr  
  115                        120                        125  
  
 Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His  
  130                        135                        140  
  
 Arg Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu  
  145                        150                        155                        160  
  
 Val Met Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile  
  165                        170                        175  
  
 Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met  
  180                        185                        190  
  
 Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Phe Ala Gly

195	200	205
Val Asp Ala Glu Thr His Val Thr Gly Gly Ser Ala Gly His Thr Val		
210	215	220
Ser Gly Phe Val Ser Leu Leu Ala Pro Gly Ala Lys Gln Asn Val Gln		
225	230	235
Leu Ile Asn Thr Asn Gly Ser Trp His Leu Asn Ser Thr Ala Leu Asn		
245	250	255
Cys Asn Asp Ser Leu Asn Thr Gly Trp Leu Ala Gly Leu Phe Tyr His		
260	265	270
His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg		
275	280	285
Pro Leu Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn		
290	295	300
Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro Pro Lys		
305	310	315
320		
Pro Cys Gly Ile Val Pro Ala Lys Ser Val Cys Gly Pro Val Tyr Cys		
325	330	335
Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala		
340	345	350
Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val Leu Asn		
355	360	365
Asn Thr Arg Pro Pro Leu Gly Asn Trp Phe Gly Cys Thr Trp Met Asn		
370	375	380
Ser Thr Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile Gly		
385	390	395
400		
Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Phe Arg Lys		
405	410	415
His Pro Asp Ala Thr Tyr Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr		
420	425	430
Pro Arg Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys		
435	440	445
Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly Gly Val		
450	455	460
Glu His Arg Leu Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys		
465	470	475
480		
Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Thr		
485	490	495
Thr Thr Gln Trp Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala		
500	505	510
Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln		
515	520	525

Tyr Leu Tyr Gly Val Gly Ser Ser Ile Ala Ser Trp Ala Ile Lys Trp  
530 535 540

Glu Tyr Val Val Leu Leu Phe Leu Leu Ala Asp Ala Arg Val Cys  
545 550 555 560

Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu  
565 570 575

Glu Asn Leu Val Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly  
580 585 590

Leu Val Ser Phe Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly  
595 600 605

Lys Trp Val Pro Gly Ala Val Tyr Thr Phe Tyr Gly Met Trp Pro Leu  
610 615 620

Leu Leu Leu Leu Leu Ala Leu Pro Gln Arg Ala Tyr Ala  
625 630 635